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• Help Index

• General Help

• Formats

• Gaps

• Matrix

• References

• Clustalw Help

Clustalw Your results

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CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: Zlot	470 aa
Sequence 2: 98	351 aa
Sequence 3: 140	257 aa
Sequence 4: 141	257 aa
Sequence 5: 142	291 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2)	Aligned.	Score: 97
Sequences (1:3)	Aligned.	Score: 97
Sequences (1:4)	Aligned.	Score: 97
Sequences (1:5)	Aligned.	Score: 85
Sequences (2:3)	Aligned.	Score: 97
Sequences (2:4)	Aligned.	Score: 97
Sequences (2:5)	Aligned.	Score: 85
Sequences (3:4)	Aligned.	Score: 100
Sequences (3:5)	Aligned.	Score: 96
Sequences (4:5)	Aligned.	Score: 96

Guide tree file created:

Start of Multiple Alignment

[/ebi/extserv/old-work/clustalw-20030820-01221410.dnd]

<http://www.ebi.ac.uk/services/tmp/clustalw-20030820-01221410.html>

8/19/03

There are 4 groups
Aligning...
Group 1: Sequences: 2 Score:5532
Group 2: Sequences: 2 Score:7554
Group 3: Sequences: 3 Score:5539
Group 4: Sequences: 5 Score:5810
Alignment Score 16213
CLUSTAL-Alignment file created [/ebi/extserv/old-work/clustalw-20030820-01221410.aln]

You

clustalw-20030820-01221410.aln

CLUSTAL W (1.82) multiple sequence alignment

```

Zlot
98      MGIWTS GTDIFLSLWEIYVSPRSPGWMDFIQHLGVCCCLVALISVGLLSVAACWFLPSIIA 60
140     -----MDFIQHLGVCCCLVALISVGLLSVAACWFLPSIIA 34
141     -----MDFIQHLGVCCCLVALISVGLLSVAACWFLPSIIA 34
142     -----MDFIQHLGVCCCLVALISVGLLSVAACWFLPSIIA 34
          *****
          *****

Zlot
98      AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 120
140     AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 94
141     AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 94
142     AAASWIIITCVLLCCSKHARCFILLVFLSCGLREGRNALIAAGTGIVILGHVENIFHNFKG 94
          *****
          *****

Zlot
98      LLDGMTCNLRAKFSIHFPLLKKYIEAIQWIYGLATPLSVFDDLVSWNQTLAVSLFSPSH 180
140     LLDGMTCNLRAKFSIHFPLLKKYIEAIQWIYGLATPLSVFDDLVSWNQTLAVSLFSPSH 154
141     LLDGMTCNLRAKFSIHFPLLKKYIEAIQWIYGLATPLSVFDDLVSWNQTLAVSLFSPSH 154
142     LLDGMTCNLRAKFSIHFPLLKKYIEAIQWIYGLATPLSVFDDLVSWNQTLAVSLFSPSH 154
          *****
          *****

Zlot
98      VLEAQLNDSKGEVLSVLYQMATTTEVLSLQKLLAFAGLSLVLLGTGLFMKRFLGPCGW 240
140     VLEAQLNDSKGEVLSVLYQMATTTEVLSLQKLLAFAGLSLVLLGTGLFMKRFLGPCGW 214
141     VLEAQLNDSKGEVLSVLYQMATTTEVLSLQKLLAFAGLSLVLLGTGLFMKRFLGPCGW 214
142     VLEAQLNDSKGEVLSVLYQMATTTEVLSLQKLLAFAGLSLVLLGTGLFMKRFLGPCGW 214
          *****
          *****
```

```
Zlot
98 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRKYVVIPTFWPTPKERNLGLFFLPI 300
140 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRKYVVIPTFWPTPKERNLGLFFLPI 274
141 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRKFISG----- 254
142 KYENIYITRQFVQFDERERHQORPCVLP LNKEERRK----- 250
      KYENIYITRQFVQFDERERHQORPCMLP LNKEERRKNKEL----- 254
      *****;*****

Zlot
98 LIHLCIWVLF AAVDYLLYRLIFSVSKQFQSLPGFEVHLKLHGEKQGTQDI IHDSSFNISV 360
140 LIHLCIWVL -AAVDYLLYRLIFSVSKQFQSLPGFEVHLKLHGEKQGTQDI IHDSSFNISV 333
141 -----FQS----- 257
142 -----KILSMILPLIYLC LNPTVSONQNSFYLRPGFLSV 288
      -----FISGFQS- 257

Zlot
98 FEPNCIPKPKFLLSETWVPLSVILLILVMLGLSSILMQLKILVSASFYPSVERKRIQYL 420
140 FEPNCIPKP-----WQALKLLAH----- 351
141 -----
142 LFF----- 291

Zlot
98 HAKLLKKRSKQPLGEVKRRLSLYLTKIHFWLPV LKMKIRKQMDMASADKS 470
140 -----
141 -----
142 -----
```

clustalw-20030820-01221410.dnd

```
(
(
(
Zlot:0.01282,
98:0.01282)
:0.03591,
140:-0.02149)
:0.02149,
141:-0.02149,
```

142:0.05262);



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